AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

Listing Of Claims

1.   (Currently amended)   A composition comprising a protein in crystalline form, wherein ~~at least a portion of~~ the protein ~~has at least 90% identity with residues 51-778 of SEQ. ID No. 1~~ consists of SEQ. ID No. 3.

2-3.   (Cancelled)

4.   (Currently amended) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution ~~greater~~ less than 3.0 Angstroms.

5.   (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

6.   (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$.

7.   (Currently amended) A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising[:] a precipitant solution and a protein ~~wherein at least a portion of the protein has at least 90% identity with residues 51-778 of SEQ. ID No. 1~~ that consists of SEQ. ID No. 3; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

8.   (Currently amended) A method according to claim 7 wherein ~~at least a portion of~~ the protein ~~has at least 95% identity with residues 51-778 of SEQ. ID No. 1~~ is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

9.   (Cancelled)

10.   (Currently amended) A method according to claim 7 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution ~~greater~~ less than 3.0 Angstroms.

11.   (Original) A method according to claim 7 wherein the protein crystal has a crystal lattice in a P21 space group.

12.   (Original) A method according to claim 7 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$.

13.   (Original) A method according to claim 7, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

14.   (Cancelled)

15.   (Currently amended) A composition according to claim ~~14~~ 16 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

16.   (Currently amended) A composition comprising ~~an isolated~~ a protein consisting of SEQ. ID No. 3.

17.   (Currently amended) A method of identifying an entity that associates with a protein, comprising:

        taking structure coordinates from diffraction data obtained from a <u>protein crystal formed according to the method of claim 7;</u> ~~has at least 90% identity with SEQ. ID No. 3;~~ and

        performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

18.   (Currently amended)   A method according to claim 17 wherein the protein <u>from which the protein crystal is formed</u> ~~has at least 95% identity with SEQ. ID No. 3.~~ <u>is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.</u>

19.   (Original) A method according to claim 17 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$.

20.   (Original) A method according to claim 17, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

21.   (Original) A method according to claim 17, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

22-23. (Cancelled)